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OM protein - protein search, using sw model

Run on: June 3, 2003, 15:02:13 ; Search time: 83 Seconds
Perfect score: 1274 (without alignments)
Sequence: 1 MYSKGEELFTGTVFILVLD.....YULGFYTAAAGITLGMDELYK 239
593.316 Million cell updates/sec

Title: US-09-887-784-4
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRIMBL_21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_minc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodont:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirnus:
16: sp_bacteriap:
17: sp_archeap:

SPTRIMBL_21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_minc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodont:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirnus:
16: sp_bacteriap:
17: sp_archeap:

17 238.5 18.7 266 5 Q9u6Y3
18 232 18.2 225 5 Q8t5F1
19 209 16.4 234 5 Q8t5F2
20 208.5 16.4 229 5 Q9u6Y6
21 205 16.2 227 5 Q962P9
22 205.5 16.1 221 5 Q9GP5
23 204 16.0 221 5 Q95P04
24 203.5 16.0 238 5 Q9BLX9
25 202 15.9 227 5 Q95vT0
26 201.5 15.8 225 5 Q9u6Y8
27 201.5 15.8 232 5 Q9GZ28
28 198.5 15.6 225 5 Q8t6T9
29 198 15.5 235 5 Q8t5F0
30 197.5 15.5 232 5 Q9u6Y7
31 188.5 14.8 227 5 Q95wB5
32 187.5 14.7 228 5 Q9GPi6
33 187 14.5 230 5 Q9tGJ7
34 184.5 14.5 233 5 Q963I9
35 183.5 14.4 238 5 Q9BLZ0
36 180.5 14.2 227 5 Q95wB6
37 174.5 13.7 227 5 Q95W11
38 172.5 13.5 231 5 Q9u6Y5
39 170.5 13.4 229 5 Q8t5e7
40 168.5 13.2 231 5 Q8t5E8
41 166 13.0 231 5 Q9u6Y4
42 161 12.6 234 5 Q8t5F3
43 158.5 12.4 231 5 Q8t4U4
44 150 11.8 231 5 Q8t5T8
45 143 11.2 231 5 Q8t5E9

ALIGNMENTS

RESULT 1
Q93125 PRELIMINARY; PRT; 238 AA.
ID Q93125
AC 01-FBB-1997 (TREMBREL_02, Created)
DT 01-FBB-1997 (TREMBREL_02, Last sequence update)
DT 01-JUN-2002 (TREMBREL_21, Last annotation update)
DE Green fluorescent protein mutant 3.
GN GFP.
OS Aequorea victoria (Jellyfish).
OC Eukaryota; Metzoa; Cnidaria; Hydrozoa; Leptomedusae;
OC Aequorea; Aequorea.
RN [1]
RN SEQUENCE FROM N.A.; PubMed=8707053;
RX CORNACK B.P.; VALIDVIA R.H.; FALKOW S.;
RA "PACS-Optimized mutants of the green fluorescent protein (GFP)." ;
RL Gene 173:33-38(1995).
RN [2]
RN SEQUENCE FROM N.A.
RA CORNACK B.P.; BERTRAM G.; EGERTON M.; GOW N.A.R.; FALKOW S.;
RA BROWN A.J.P.;
RT "Yeast Enhanced Green Fluorescent Protein (YEGFP): a reporter of gene expression in *Candida albicans*." ;
EMBL: U73001; AAB18057.1; -.
HSSP: P42212; 1BEP
INTERPRO: IPR00786; Green_fl_protein.
PFAM: PF01353; GFP; 1.
PRINTS: PRO1229; GFLUORESCENT.
DR PRODOM; PDD013756; Green_fl_protein; 1.
SEQUENCE 238 AA; 26840 MW; A28622809A9DEA60 CRC64;
SQ

Query Match Score 97.3%; Score 1240; DB 5; Length 238;
Best Local Similarity 97.5%; Pred. No. 1..3..94;
Matches 232; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Result %
No. Score Query Match Length DB ID Description
1 1240 97.3 238 5 Q93125 aequorea vi
2 1239 97.3 238 5 Q27903 unidentified
3 1227 96.3 238 5 Q96JQ1 homo sapien
4 1205 94.6 238 5 Q17105 aequorea vi
5 1190 93.4 238 5 Q17106 aequorea vi
6 1085 95.2 238 5 Q8WTC6 aequorea ma
7 1081 84.9 238 5 Q8WTC5 aequorea ma
8 1077 84.5 238 5 Q8WTC4 aequorea ma
9 1075 84.4 238 5 Q8WTD0 aequorea ma
10 1074 84.3 238 5 Q8WTC9 aequorea ma
11 1072 84.1 238 5 Q8WTC8 aequorea ma
12 1072 84.0 238 5 Q8WTC7 aequorea ma
13 1070 84.0 238 5 Q8WTC5 aequorea ma
14 252.5 19.8 225 5 Q95uA7 montastraea
15 247 19.4 225 5 Q963F5 montastraea
16 244.5 19.2 236 5 Q8t6U0 dendronept

2 VSKGEELFTGTVFILVLDGVPILVPLFGRKLPVPMPTL 61

Db	1	MSKGSEELFIGVQFSRYPDHMKHDFPSKAMPEGYVORTIFFKDDGNYKTRAEVKFEGDTLV	60	Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.
	OC			OC Mammalia; Butcheria; -
Qy	62	VTTLSYGQFSRYPDHMKHDFPSKAMPEGYVORTIFFKDDGNYKTRAEVKFEGDTLV	121	NCBI_TAXID:9606;
	61	VTTFSYGQFSRYPDHMKHDFPSKAMPEGYVORTIFFKDDGNYKTRAEVKFEGDTLV	120	RN SEQUENCE FROM N.A.
Db	122	NRIEKGIDKEGNILGHKEYNNNSHVNIMADKQNSIKVNFKIRHNIEDGSYQLAD	181	RC TISSUE-SPLEEN;
	121	NRIEKGIDKEGNILGHKEYNNNSHVNIMADKQNSIKVNFKIRHNIEDGSYQLAD	180	RX PubMed:11429608;
Qy	182	HYQQNTPIGDGPVLLPDNYLSTQALSBDPNEKRDHMVLGLFTYAAGITLGMDFLYK	239	RA Mochizuki, N.; Yamashita, S.; Kurokawa, K.; Ohba, Y.; Nagai, T.; Miyawaki, A.; Matsuda, M.; -
	181	HYQQNTPIGDGPVLLPDNYLSTQALSBDPNEKRDHMVLGLFTYAAGITHGMDFLYK	238	RT Spatio-temporal Images of Growth Factor-induced Activation of Ras and Rap1*;
Db	RESULT 2			RT Nature 411:1065-1068(2001);
	ID Q27903	PRELIMINARY;	PRTR; 238 AA.	RL Nature 411:1065-1068(2001);
AC	Q27903;			DR AB051846; BAB61868.1; -
	DT 01-NOV-1996	(TREMBLrel. 01; Created)		DR InterPro: IPR00786; Green_f1_protein.
RA	Rowland G.J.A.; Mendes O.; Wobert B.J.H.; de Boer A.D.;			DR InterPro: IPR001806; Ras_transfrrmg.
	RT *Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage. ;			DR InterPro: IPR003116; RBD.
RL	Plant Mol. Biol.	33:989-999(1997).		DR InterPro: IPR005225; Small_GTP.
	DR	X66418; CAA5278.1; -		DR Pfam: PF01153; GFP; 2.
DR	HSSP:	P42212; 1GFL		DR Pfam: PF02196; RBD; 1.
	DR	InterPro: IPR00786; Green_f1_protein.		DR Prod: P0013756; Green_f1_protein; 2.
DE	Green fluorescent protein.			DR TIGRFAMs; TIGR0031; small_GTP; 1.
	GN			DR PROSITE; PS00294; PRENYLATION; UNKOWN_1.
OS	unidentified.			DR GTP-binding.
	OC			KW KW 8612408F607CFD49 CRC64;
NCB_I-TAXID=34644;	OX			SQ SEQUENCE 758 AA; 85015 MW;
	RN	[1]		Query Match 96.3%; Score 1227; DB 4; Length 758;
RP	SEQUENCE FROM N.A.			Best Local Similarity 97.5%; Pred. No. 6.9e-93;
	RX	MEDLINE-979382; PubMed=9154981;		Matches 231; Conservative 2; MisMatches 4; Indels 0; Gaps 0;
RA	Rouwendal G.J.A.; Mendes O.; Wobert B.J.H.; de Boer A.D.;			Qy 1 MYSKGEELFTGVPVPLVLDGVNGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
	RT	*Enhanced expression in tobacco of the gene encoding green fluorescent protein by modification of its codon usage. ;		60 DR 498 MYSKGEELFTGVPVPLVLDGVNGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
RL	Plant Mol. Biol.	33:989-999(1997).		DR 61 LYTTLSGVQCFSPRYPDHMKQHDFEKSAMPEGVYQERTIFKDGGNYKTRAEVKFEGDTL
	DR	X66418; CAA5278.1; -		DR 62 LYTTLTGQVQCFSPRYPDHMKQHDFEKSAMPEGVYQERTIFKDGGNYKTRAEVKFEGDTL
DR	HSSP:	P42212; 1GFL		DR 63 1VRIELGIDFEKDGTLNLGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
	DR	InterPro: IPR00786; Green_f1_protein.		DR 64 1VRIELGIDFEKDGTLNLGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
DR	PFAM: P01353; GFP; 1.			DR 65 1VRIELGIDFEKDGTLNLGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
	DR	PRINTS: PRO1229; GFLUORESCENT.		DR 66 1VRIELGIDFEKDGTLNLGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
DR	PRODOM: PD013756; Green_f1_protein; 1.			DR 67 1VRIELGIDFEKDGTLNLGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
	SEQUENCE 238 AA;	c932d47262af2d3	CRC64;	DR 68 1VRIELGIDFEKDGTLNLGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD
SO	2	VSKGEELFTGVPVPLVLDGVNGHKEYNNNSHVNIMADRKQNSIKVNFKIRHNIEDGSYQLAD	61	RESULT 4
	1	MKGSEELFIGVQFSRYPDHMKHDFPSKAMPEGYVORTIFFKDDGNYKTRAEVKFEGDTLV	60	Q17105 PRELIMINARY; PRT; 238 AA.
Db	62	VTTLSYGQFSRYPDHMKHDFPSKAMPEGYVORTIFFKDDGNYKTRAEVKFEGDTLV	121	AC Q17105 PRELIMINARY; PRT; 238 AA.
	61	VTTFSYGQFSRYPDHMKHDFPSKAMPEGYVORTIFFKDDGNYKTRAEVKFEGDTLV	120	AC Q17105 PRELIMINARY; PRT; 238 AA.
Qy	122	NRIEKGIDKEGNILGHKEYNNNSHVNIMADKQNSIKVNFKIRHNIEDGSYQLAD	181	AC Q17105 PRELIMINARY; PRT; 238 AA.
	121	NRIEKGIDKEGNILGHKEYNNNSHVNIMADKQNSIKVNFKIRHNIEDGSYQLAD	180	AC Q17105 PRELIMINARY; PRT; 238 AA.
Db	182	HYQQNTPIGDGPVLLPDNYLSTQALSBDPNEKRDHMVLGLFTYAAGITLGMDFLYK	239	AC Q17105 PRELIMINARY; PRT; 238 AA.
	181	HYQQNTPIGDGPVLLPDNYLSTQALSBDPNEKRDHMVLGLFTYAAGITLGMDFLYK	238	AC Q17105 PRELIMINARY; PRT; 238 AA.
Qy	183	RAICHU40X.		AC Q17105 PRELIMINARY; PRT; 238 AA.
	DB	RAICHU40X.		AC Q17105 PRELIMINARY; PRT; 238 AA.
Db	RESULT 3			AC Q17105 PRELIMINARY; PRT; 238 AA.
	Q965Q1	PRELIMINARY;	PRTR; 758 AA.	AC Q17105 PRELIMINARY; PRT; 238 AA.
AC	Q965Q1;			AC Q17105 PRELIMINARY; PRT; 238 AA.
	DR	01-DEC-2001 (TREMBLrel. 19; Created)		AC Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
DR	01-DEC-2001 (TREMBLrel. 19; Last sequence update)			DR EMBL: X83951; CLAS878.1; -
	DT	01-JUN-2002 (TREMBLrel. 21; Last annotation update)		DR HSSP: P42212; GFL.
Qy	184	RAICHU40X.		DR InterPro: IPR00786; Green_f1_protein.
	DB	RAICHU40X.		DR Pfam: PF01153; GFP; 1.
DR	RAICHU40X.			DR Prints: PRO13756; Green_f1_protein; 1.
	NON_TER			DR Prod: P013756; Green_f1_protein; 1.
FT	RAICHU40X.			DR FT 238

SQ	SEQUENCE	238 AA;	26950 MW;	26E2BE450E748E44 CRC64;	
Query Match	Score 94.6%;	Score 1205;	DB 5;	Length 238;	
Best Local Similarity	94.1%;	Pred. No. 9.8e-92;			
Matches 224; Conservative 6; Mismatches 8; Indels 0;					
Qy	2 VSKGEELFTGVPPILVEDGVDNGHFKFSVSESEGEGDATYGKLTKFCTTGKLKPVPWPML 61 : : : : : : : : : : : : : 1 MSKGEELFTGVPPILVEDGVDNGHFKFSVSESEGEGDATYGKLTKFCTTGKLKPVPWPML 60				
Db					
Qy	62 VTTLSYGVCQCFSRYPDHMKQHDFFKSFAMPEGYVQETIFFKDDGNYKTRAEVKFEGDTLV 121 : : : : : : : : : : : : : 61 VTFSTSGVQCFSRYPDHMKQHDFFKSFAMPEGYVQETIFFKDDGNYKTRAEVKFEGDTLV 120				
Db					
Qy	122 NRIELKGIDFEDGNLIGHKLEY NYNSHNYYIMADKQNGKIKVNKFTRHNTEDGSVQLAD 181 : : : : : : : : : : : : : 121 NRIELKGIDFEDGNLIGHKLEY NYNSHNYYIMGDPKNGKIKVNKFTRHNTEDGSVQLAD 180				
Db					
Qy	182 HYQONTPIGDGPVLLPDNHYLSTS QASLSKDPNEKRDHMVLGFVTAAGITLGMDELYK 239 : : : : : : : : : : : : : 181 HYQONTPIGDGPVLLPDNHYLSTS QASLSKDPNEKRDHMVLGFVTAAGITLGMDELYK 238				
Db					
RESULT 5					
Q17106	PRELIMINARY;	PRT;	238 AA.		
ID	Q17106;				
AC	Q17106;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Green fluorescent protein (Fragment).				
GN					
RN					
OS	Aequorea victoria (Jellyfish).				
RA	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Leptomedusae;				
OC	Aequorididae; Aequorea.				
OX					
NCBI_TAXID=6100;					
RP	SEQUENCE FROM N.A.				
RA	Watkins J.N.; Campbell A.K.;				
RL	Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.				
DR	X83966; CA58790.1; -.				
RSP;	P42212; 1BPP.				
DR	InterPro: IPR000786; Green_fl_protein.				
DR	Pfam; PF01353; GFP; 1.				
DR	PRINTS; PRO13756; GFP; 1.				
DR	PRODOM; PD013756; Green_fl_protein; 1.				
FT	NON_TER 238 AA;	28867 MW;	ED4649262DBEABD4 CRC64;		
SQ	SEQUENCE	238 AA;	28867 MW;	ED4649262DBEABD4 CRC64;	
Query Match	Score 93.4%;	Score 1190;	DB 5;	Length 238;	
Best Local Similarity	93.3%;	Pred. No. 1.7e-90;			
Matches 222; Conservative 222; Mismatches 7; Indels 0; Gaps 0;					
Qy	2 VSKGEELFTGVPPILVEDGVDNGHFKFSVSESEGEGDATYGKLTKFCTTGKLKPVPWPML 61 : : : : : : : : : : : : : 1 MSKGEELFTGVPPILVEDGVDNGHFKFSVSESEGEGDATYGKLTKFCTTGKLKPVPWPML 60				
Db					
Qy	62 VTTLSYGVCQCFSRYPDHMKQHDFFKSFAMPEGYVQETIFFKDDGNYKTRAEVKFEGDTLV 121 : : : : : : : : : : : : 61 VTTLSYGVCQCFSRYPDHMKQHDFFKSFAMPEGYVQETIFFKDDGNYKTRAEVKFEGDTLV 120				
Db					
Qy	122 NRIELKGIDFEDGNLIGHKLEY NYNSHNYYIMADKQNGKIKVNKFTRHNTEDGSVQLAD 181. : : : : : : : : : : : : 121 NRIELKGIDFEDGNLIGHKLEY NYNSHNYYIMGDPKNGKIKVNKFTRHNTEDGSVQLAD 180				
Db					
Qy	182 HYQONTPIGDGPVLLPDNHYLSTS QASLSKDPNEKRDHMVLGFVTAAGITLGMDELYK 239 : : : : : : : : : : : : 181 HYQONTPIGDGPVLLPDNHYLSTS QASLSKDPNEKRDHMVLGFVTAAGITLGMDELYK 238				
Db					
RESULT 6					
Q8WTC6	PRELIMINARY;	PRT;	238 AA.		
ID	Q8WTC6				
Query Match	Score 84.9%;	Score 1081;	DB 5;	Length 238;	
Best Local Similarity	81.9%;	Pred. No. 1.7e-81;			

QY	2	VSKGEELFETGVVPILVLDGVNCHKFSVSCEGGDATYGKLTKFICCTGKLPPWPTL 61	GN	GFP.
Db	1	MSKGEELFTGIVPVLDGVNCHKFSVSCEGGDATYGKLPPWPTL 60	OS	Eukaryota; macrodactyla.
QY	62	VTTLSYGQCSRPDHMKHDFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLV 121	OC	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.
Db	61	VTTLGIGQCFARYEHMKMDFKSAMPEGYIQERTIFFQDGKTKTRGEVKFEGDTLV 120	NCBI_TaxID	147615;
QY	122	NRIELKGIDFKEGNILGHKLEYNNNSHNYYIMADRKONGIKVNFKIRHNTEDGVQLAD 181	RN	[1]
Db	121	NRIELKGMDFKEGNILGHKLEYNFISHNYTIMPDRANGLKVNEKIRHNTEDGVQLAD 180	SEQUENCE	FROM N.A.
QY	182	HYQQNTPIGDPVLPDNPYLSTOSALSKDNEKRHDMLLGFTAAAGITLGMDLYK 239	STRAIN	GPXM19UV;
Db	181	HYOTNVPLGDGPVLPINHYSQTAISKDRNETRDHMVLEFFSACGHTHGMDELYK 238	RC	"Colorful mutants of green fluorescent protein from Aequorea macrodactyla."
GN		Submitted (OCT 2001) to the EMBL/GenBank/DBBJ databases.	RA	Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;
OS		macrodactyla.	RT	"Colorful mutants of green fluorescent protein from Aequorea macrodactyla."
OC		EMBL: AF435430; AAL33915; 1; -	RL	Submitted (OCT 2001) to the EMBL/GenBank/DBBJ databases.
OC		InterPro: IPR000786; Green_fl_protein.	DR	DR ProDom: PD013746; Green_fl_protein; 1.
OC		PFam: PF01353; GFP; 1.	DR	DR Sequence: 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
QWTC8	RESULT 11	PRELIMINARY; PRT; 238 AA.	SQ	SEQUENCE: 238 AA; 27002 MW; BD5BA2982264C018 CRC64;
ID	Q8WTC8	PRT; 238 AA.		
AC	Q8WTC8;			
DT	01-MAR-2002	(TREMBLrel. 20, Created)		
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Green fluorescent protein.			
OS	Aequorea macrodactyla.			
EC	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.			
NCBI_TaxID	147615;			
RN	SEQUENCE FROM N.A.			
RC	STRATING-GFPXMI63;			
RA	Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;			
RA	"Colorful mutants of green fluorescent protein from Aequorea macrodactyla."			
RT	macrodactyla.			
RT	Submitted (OCT 2001) to the EMBL/GenBank/DBBJ databases.			
DR	EMBL: AF435429; AAL33914; -			
DR	InterPro: IPR000786; Green_fl_protein.			
DR	PFam: PF01353; GFP; 1.			
DR	ProDom: PD013746; Green_fl_protein; 1.			
DR	Sequence: 238 AA; 27002 MW; 5F0A018PALE7C84D CRC64;			
Q8WTC5	RESULT 13	PRELIMINARY; PRT; 238 AA.	SQ	SEQUENCE: 238 AA; 27002 MW; 5F0A018PALE7C84D CRC64;
ID	Q8WTC5	PRT; 238 AA.		
AC	Q8WTC5;	PRELIMINARY;		
DT	01-MAR-2002	(TREMBLrel. 20, Created)		
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Orange fluorescent protein.			
OS	Aequorea macrodactyla.			
OC	Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.			
NCBI_TaxID	147615;			
RN	SEQUENCE FROM N.A.			
RC	STRATING-GFPXMI63;			
RA	Luo W.X., Zhang J., Yang H.J., Xie X.Y., Li S.W., Guan B.Q., Chen M., Li S.J., Xia N.S.;			
RA	"Colorful mutants of green fluorescent protein from Aequorea macrodactyla."			
RT	Submitted (OCT 2001) to the EMBL/GenBank/DBBJ databases.			
DR	EMBL: AF435432; AAL33917; -			
DR	InterPro: IPR000786; Green_fl_protein.			
DR	PFam: PF013756; GFP; 1.			
DR	ProDom: PD013756; Green_fl_protein; 1.			
DR	Sequence: 238 AA; 27002 MW; 75521EA5534E573A CRC64;			
Q8WTC7	RESULT 12	PRELIMINARY; PRT; 238 AA.	SQ	SEQUENCE: 238 AA; 27002 MW; 75521EA5534E573A CRC64;
ID	Q8WTC7	PRT; 238 AA.		
AC	Q8WTC7;	PRELIMINARY;		
DT	01-MAR-2002	(TREMBLrel. 20, Created)		
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Green fluorescent protein.			

Db	1	MSKGEELFPTGVPILVELGDYVGHKFVSVRGEGEADYGKLEIKFICITGKLKPWPWPTL	60	RP SEQUENCE FROM N.A. RA Lesser M.P.; Barry T.M.; Mazel C.; Mattz M.V.; Lukyanov S.A., RA Falkowski P.; Gorunov M.; Kolber Z.; RT "Green fluorescent proteins in Caribbean Scleractinian corals." RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
Db	61	VTTLGIGILCFARYPEHMKMNDFFKSAMPETYQERTIFFDDGKYKTRGEVKEGDTLV	120	DR AF384603; AAC62982; 2; DR InterPro IPR00786; Green_f1_protein. DR Pram; GFP 1. DR Prodrom; PD013756; Green_f1_protein; 1.
Db	122	NRIELKGIDFKEGNILGHKLEYNNNSHNVYIMDKQNGIKYNEFKIRNIEDGSVQLAD	181	DR SEQUENCE 225 AA; 25887 MW; 770b7D7C16929AF CRC64; SQ Sequence 225 AA; 25887 MW; 770b7D7C16929AF CRC64;
Db	121	NRIELKGMDFKEDGNILGHKLEYNNNSHNVYIMDKQNGIKYNEFKIRNIEDGSVQLAD	180	Query Match 19.4%; Score 247; DB 5; Length 225; Best Local Similarity 27.6%; Pred. No. 1.1e-12; Matches 59; Conservative 42; Mismatches 85; Indels 28; Gaps 6;
Db	182	HYQQNTPIGDPVLLPDNHYLSTQSLSKDPNEKRDHVNLLGFVTAAGITLGMDELYK	239	Qy 12 VVPILVELDGDNHGKHFVSGESEGDDATGGLTLKFLCTTG-KLPVWPWTLYTTSYGVQ 70 Db 7 IMEIKLRLQMGVYNGSHKFVKGEGESKPFESTOTINUTYKEAPLFPAYDILTSAFQYGNR 66
Db	181	HYQTNPVLDGPVLIPINHYLSYQTAISKDRNETRDINVFLEPSACGTHGMDELYK	238	Qy 71 CFSSRYPDHNKQHDFKFSAMPEGYVYDERTIFKDDGNYKTRAEVKFEGDTLYNRIELKGID 130 Db 67 VFTKYPDD1P--DYFKQTKTPEGYSWERMAYEDQSICATSDIRMEGDCFYEQFGV 124
Qy	RESULT 14			Qy 131 FKEFDGNILGHK-LEYNNNSHNVYIMDKQNGIKYNEFKIRNIEDGSVOLA-----DHY 183 Db 125 FPPNGPVAQKTLKWEPESTEKMY-----VPGVLIKSDVNMALLEGHHY 169
Q950A7	ID 0950A7	PRELIMINARY; PRT; 225 AA.		Qy 184 Q---QNTPIGDPVLLPDNHYLSTQSLSKDPNE 214 Db 170 RCDFRSTYKAKRQVQLPDYHFVDRIEILSHND 203
AC	Q950A7;			Search completed: June 3, 2003, 15:08:36 Job time : 85 secs
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Cyan fluorescent protein (Fragment),			
OS	Montastraea cavernosa (great star coral).			
OC	Eukaryota; Metazoa; Cnidaria; Anthozoa; zoantharia; scleractinia; Favilina; Favidae; Montastraea.			
OX	NCBI_TAXID=63558;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Falkowski, P.G.; Sun, Y.;			
RT	"Montastraea cavernosa fluorescent protein."			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.			
DR	AY056460; AA117905 1;			
DR	InterPro IPR00786; Green_f1_protein.			
DR	Pfam; PF01353; GFP 1.			
DR	Prodrom; PD013756; Green_f1_protein; 1.			
FT	NON_TER 225			
SO	SEQUENCE 225 AA; 25775 MW; 52D5F2T16D083524 CRC64;			
Qy	RESULT 15			
Q963F5	ID Q963F5	PRELIMINARY;	PRT; 225 AA.	
AC	Q963F5;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-JUN-2002	(TREMBLrel. 19, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	Green fluorescent protein.			
OS	Montastraea cavernosa (great star coral).			
OC	Eukaryota; Metazoa; Cnidaria; Anthozoa; zoantharia; scleractinia; Favilina; Favidae; Montastraea.			
OX	NCBI_TAXID=63558;			
RN	[1]			